

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 10/686, 835A  
Source: IFW16  
Date Processed by STIC: 09/22/2005

# ***ENTERED***



IFW16

## RAW SEQUENCE LISTING

DATE: 09/22/2005

PATENT APPLICATION: US/10/686,835A

TIME: 15:15:14

Input Set : A:\sequence listing.txt

Output Set: N:\CRF4\09222005\J686835A.raw

4 <110> APPLICANT: BOEHRINGER INGELHEIM (CANADA) LTD.  
 6 <120> TITLE OF INVENTION: SELF REPLICATING RNA MOLECULE FROM  
 7 HEPATITIS C VIRUS  
 9 <130> FILE REFERENCE: 13/083  
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/686,835A  
 C--> 11 <141> CURRENT FILING DATE: 2003-10-16  
 11 <150> PRIOR APPLICATION NUMBER: 10/029,907  
 12 <151> PRIOR FILING DATE: 2001-12-21  
 14 <150> PRIOR APPLICATION NUMBER: 60/257,857  
 15 <151> PRIOR FILING DATE: 2000-12-22  
 17 <160> NUMBER OF SEQ ID NOS: 28  
 19 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
 21 <210> SEQ ID NO: 1  
 22 <211> LENGTH: 8639  
 23 <212> TYPE: DNA  
 24 <213> ORGANISM: HCV  
 26 <220> FEATURE:  
 27 <221> NAME/KEY: CDS  
 28 <222> LOCATION: (1803)...(8408)  
 30 <400> SEQUENCE: 1  
 31 ggccagcccc cgattggggg cgacactcca ccatagatca ctccccctgtg aggaactact 60  
 32 gtcttcacgc agaaagcgtc tagccatggc gttagtatga gtgtcgtgca gcctccagga 120  
 33 cccccctcc cgaggagagcc atagtgggtct gcggaaccgg tgagtacacc ggaattgcca 180  
 34 ggacgaccgg gtcctttctt ggatcaaccc gctcaatgcc tggagatttg ggcgtgcccc 240  
 35 cgcgagactg ctagccgagt agtggtgggt cgcgaaaggc cttgtggtac tgcctgatag 300  
 36 ggtgcttgcg agtgccccgg gaggtctcgt agaccgtgca ccatgagcac gaatcctaaa 360  
 37 cctcaaagaa aaaccaaagg gcgcgcctatg attgaacaag atggattgca cgcaggttct 420  
 38 ccggccgctt ggggtggagag gctattcggc tatgactggg cacaacagac aatcggctgc 480  
 39 tctgatgccg ccgtgttccg gctgtcagcg caggggcgcc cggttctttt tgtcaagacc 540  
 40 gacctgtccg gtgccctgaa tgaactgcag gacgaggcag cgcggctatc gtggctggcc 600  
 41 acgacgggcg ttccttgccg agctgtgctc gacgttgctc ctgaagcggg aagggaactgg 660  
 42 ctgctatttg gcgaagtgcc ggggcaggat ctctgtcat ctacacttgc tcctgccgag 720  
 43 aaagtatcca tcatggctga tgcaatgcgg cggctgcata cgcttgatcc ggctacctgc 780  
 44 ccattcgacc accaagcgaa acatcgcac gagcgagcac gtactcggat ggaagccggg 840  
 45 cttgtcgatc aggatgatct ggacgaagag catcaggggc tcgcgccagc cgaactgttc 900  
 46 gccaggctca aggcgcgcac gcccgacggc gaggatctcg tcgtgaccca tggcgatgcc 960  
 47 tgcttgccga atatcatggg ggaatggc cgcttttctg gattcatcga ctgtggccgg 1020  
 48 ctgggtgtgg cggaccgcta tcaggacata gcgttggtc cccgtgatat tgctgaagag 1080  
 49 cttggcggcg aatgggctga ccgcttcctc gtgctttacg gtatcgccgc tcccgattcg 1140  
 50 cagcgcacgc ccttctatcg ccttcttgac gagttcttct gagttcgcgc ccagatgtta 1200  
 51 acagaccaca acggtttccc tctagcggga tcaattccgc cccccccct aacgttactg 1260  
 52 gccgaagccg cttggaataa ggccggtgtg cgtttgctc tatgttattt tccaccatat 1320  
 53 tgccgtcttt tggcaatgtg agggcccgga aacctggccc tgtcttcttg acgagcattc 1380

(Pg. 6)

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54 ctaggggtct tccccctctc gccaaaggaa tgcaagggtct gttgaatgtc gtgaaggaag 1440
55 cagttcctct ggaagcttct tgaagacaaa caacgtctgt agcgaccctt tgcaggcagc 1500
56 ggaaccccc acctggcgac aggtgcctct gcggccaaaa gccacgtgta taagatacac 1560
57 ctgcaaaggc ggcacaaccc cagtgccacg ttgtgagttg gatagttgtg gaaagagtca 1620
58 aatggctctc ctcaagcgta ttcaacaagg ggctgaagga tgcccagaag gtacccatt 1680
59 gtatgggata tgatctgggg cctcgggtgca catgctttac atgtgtttag tgcagggttaa 1740
60 aaaacgtcta ggccccccga accacgggga cgtgggtttc ctttgaaaaa cacgataata 1800
61 cc atg gac cgg gag atg gca gca tcg tgc gga ggc gcg gtt ttc gta 1847
62 Met Asp Arg Glu Met Ala Ala Ser Cys Gly Gly Ala Val Phe Val
63 1 5 10 15
65 ggt ctg ata ctc ttg acc ttg tca ccg cac tat aag ctg ttc ctc gct 1895
66 Gly Leu Ile Leu Leu Thr Leu Ser Pro His Tyr Lys Leu Phe Leu Ala
67 20 25 30
69 agg ctc ata tgg tgg tta caa tat ttt atc acc agg gcc gag gca cac 1943
70 Arg Leu Ile Trp Trp Leu Gln Tyr Phe Ile Thr Arg Ala Glu Ala His
71 35 40 45
73 ttg caa gtg tgg atc ccc ccc ctc aac gtt cgg ggg ggc cgc gat gcc 1991
74 Leu Gln Val Trp Ile Pro Pro Leu Asn Val Arg Gly Gly Arg Asp Ala
75 50 55 60
77 gtc atc ctc ctc acg tgc gcg atc cac cca gag cta atc ttt acc atc 2039
78 Val Ile Leu Leu Thr Cys Ala Ile His Pro Glu Leu Ile Phe Thr Ile
79 65 70 75
81 acc aaa atc ttg ctc gcc ata ctc ggt cca ctc atg gtg ctc cag gct 2087
82 Thr Lys Ile Leu Leu Ala Ile Leu Gly Pro Leu Met Val Leu Gln Ala
83 80 85 90 95
85 ggt ata acc aaa gtg ccg tac ttc gtg cgc gca cac ggg ctc att cgt 2135
86 Gly Ile Thr Lys Val Pro Tyr Phe Val Arg Ala His Gly Leu Ile Arg
87 100 105 110
89 gca tgc atg ctg gtg cgg aag gtt gct ggg ggt cat tat gtc caa atg 2183
90 Ala Cys Met Leu Val Arg Lys Val Ala Gly Gly His Tyr Val Gln Met
91 115 120 125
93 gct ctc atg aag ttg gcc gca ctg aca ggt acg tac gtt tat gac cat 2231
94 Ala Leu Met Lys Leu Ala Ala Leu Thr Gly Thr Tyr Val Tyr Asp His
95 130 135 140
97 ctc acc cca ctg cgg gac tgg gcc cac gcg ggc cta cga gac ctt gcg 2279
98 Leu Thr Pro Leu Arg Asp Trp Ala His Ala Gly Leu Arg Asp Leu Ala
99 145 150 155
101 gtg gca gtt gag ccc gtc gtc ttc tct gat atg gag acc aag gtt atc 2327
102 Val Ala Val Glu Pro Val Val Phe Ser Asp Met Glu Thr Lys Val Ile
103 160 165 170 175
105 acc tgg ggg gca gac acc gcg gcg tgt ggg gac atc atc ttg ggc ctg 2375
106 Thr Trp Gly Ala Asp Thr Ala Ala Cys Gly Asp Ile Ile Leu Gly Leu
107 180 185 190
109 ccc gtc tcc gcc cgc agg ggg agg gag ata cat ctg gga ccg gca gac 2423
110 Pro Val Ser Ala Arg Arg Gly Arg Glu Ile His Leu Gly Pro Ala Asp
111 195 200 205
113 agc ctt gaa ggg cag ggg tgg cga ctc ctc gcg cct att acg gcc tac 2471
114 Ser Leu Glu Gly Gln Gly Trp Arg Leu Leu Ala Pro Ile Thr Ala Tyr
115 210 215 220

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117	tcc	caa	cag	acg	cga	ggc	cta	ctt	ggc	tgc	atc	atc	act	agc	ctc	aca	2519
118	Ser	Gln	Gln	Thr	Arg	Gly	Leu	Leu	Gly	Cys	Ile	Ile	Thr	Ser	Leu	Thr	
119		225					230					235					
121	ggc	cgg	gac	agg	aac	cag	gtc	gag	ggg	gag	gtc	caa	gtg	gtc	tcc	acc	2567
122	Gly	Arg	Asp	Arg	Asn	Gln	Val	Glu	Gly	Glu	Val	Gln	Val	Val	Ser	Thr	
123	240					245					250					255	
125	gca	aca	caa	tct	ttc	ctg	gcg	acc	tgc	gtc	aat	ggc	gtg	tgt	tgg	act	2615
126	Ala	Thr	Gln	Ser	Phe	Leu	Ala	Thr	Cys	Val	Asn	Gly	Val	Cys	Trp	Thr	
127					260					265						270	
129	gtc	tat	cat	ggt	gcc	ggc	tca	aag	acc	ctt	gcc	ggc	cca	aag	ggc	cca	2663
130	Val	Tyr	His	Gly	Ala	Gly	Ser	Lys	Thr	Leu	Ala	Gly	Pro	Lys	Gly	Pro	
131				275					280					285			
133	atc	acc	caa	atg	tac	acc	aat	gtg	gac	cag	gac	ctc	gtc	ggc	tgg	caa	2711
134	Ile	Thr	Gln	Met	Tyr	Thr	Asn	Val	Asp	Gln	Asp	Leu	Val	Gly	Trp	Gln	
135		290						295					300				
137	gcg	ccc	ccc	ggg	gcg	cgt	tcc	ttg	aca	cca	tgc	acc	tgc	ggc	agc	tcg	2759
138	Ala	Pro	Pro	Gly	Ala	Arg	Ser	Leu	Thr	Pro	Cys	Thr	Cys	Gly	Ser	Ser	
139	305					310					315						
141	gac	ctt	tac	ttg	gtc	acg	agg	cat	gcc	gat	gtc	att	ccg	gtg	cgc	cgg	2807
142	Asp	Leu	Tyr	Leu	Val	Thr	Arg	His	Ala	Asp	Val	Ile	Pro	Val	Arg	Arg	
143	320				325					330						335	
145	cgg	ggc	gac	agc	agg	ggg	agc	cta	ctc	tcc	ccc	agg	ccc	gtc	tcc	tac	2855
146	Arg	Gly	Asp	Ser	Arg	Gly	Ser	Leu	Leu	Ser	Pro	Arg	Pro	Val	Ser	Tyr	
147				340					345							350	
149	ttg	aag	ggc	tct	tcg	ggc	ggt	cca	ctg	ctc	tgc	ccc	tcg	ggg	cac	gct	2903
150	Leu	Lys	Gly	Ser	Ser	Gly	Gly	Pro	Leu	Leu	Cys	Pro	Ser	Gly	His	Ala	
151			355					360						365			
153	gtg	ggc	atc	ttt	cgg	gct	gcc	gtg	tgc	acc	cga	ggg	ggt	gcg	aag	gcg	2951
154	Val	Gly	Ile	Phe	Arg	Ala	Ala	Val	Cys	Thr	Arg	Gly	Val	Ala	Lys	Ala	
155		370					375						380				
157	gtg	gac	ttt	gta	ccc	gtc	gag	tct	atg	gaa	acc	act	atg	cgg	tcc	ccg	2999
158	Val	Asp	Phe	Val	Pro	Val	Glu	Ser	Met	Glu	Thr	Thr	Met	Arg	Ser	Pro	
159	385					390					395						
161	gtc	ttc	acg	gac	aac	tcg	tcc	cct	ccg	gcc	gta	ccg	cag	aca	ttc	cag	3047
162	Val	Phe	Thr	Asp	Asn	Ser	Ser	Pro	Pro	Ala	Val	Pro	Gln	Thr	Phe	Gln	
163	400				405						410					415	
165	gtg	gcc	cat	cta	cac	gcc	cct	act	ggt	agc	ggc	aag	agc	act	aag	gtg	3095
166	Val	Ala	His	Leu	His	Ala	Pro	Thr	Gly	Ser	Gly	Lys	Ser	Thr	Lys	Val	
167				420					425							430	
169	ccg	gct	gcg	tat	gca	gcc	caa	ggg	tat	aag	gtg	ctt	gtc	ctg	aac	ccg	3143
170	Pro	Ala	Ala	Tyr	Ala	Ala	Gln	Gly	Tyr	Lys	Val	Leu	Val	Leu	Asn	Pro	
171				435				440								445	
173	tcc	gtc	gcc	gcc	acc	cta	ggt	ttc	ggg	gcg	tat	atg	tct	aag	gca	cat	3191
174	Ser	Val	Ala	Ala	Thr	Leu	Gly	Phe	Gly	Ala	Tyr	Met	Ser	Lys	Ala	His	
175		450					455						460				
177	ggt	atc	gac	cct	aac	atc	aga	acc	ggg	gta	agg	acc	atc	acc	acg	ggt	3239
178	Gly	Ile	Asp	Pro	Asn	Ile	Arg	Thr	Gly	Val	Arg	Thr	Ile	Thr	Thr	Gly	
179	465					470					475						
181	gcc	ccc	atc	acg	tac	tcc	acc	tat	ggc	aag	ttt	ctt	gcc	gac	ggt	ggt	3287

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182	Ala	Pro	Ile	Thr	Tyr	Ser	Thr	Tyr	Gly	Lys	Phe	Leu	Ala	Asp	Gly	Gly	
183	480					485					490					495	
185	tgc	tct	ggg	ggc	gcc	tat	gac	atc	ata	ata	tgt	gat	gag	tgc	cac	tca	3335
186	Cys	Ser	Gly	Gly	Ala	Tyr	Asp	Ile	Ile	Ile	Cys	Asp	Glu	Cys	His	Ser	
187					500					505					510		
189	act	gac	tcg	acc	act	atc	ctg	ggc	atc	ggc	aca	gtc	ctg	gac	caa	gcg	3383
190	Thr	Asp	Ser	Thr	Thr	Ile	Leu	Gly	Ile	Gly	Thr	Val	Leu	Asp	Gln	Ala	
191					515					520					525		
193	gag	acg	gct	gga	gcg	cga	ctc	gtc	gtg	ctc	gcc	acc	gct	acg	cct	ccg	3431
194	Glu	Thr	Ala	Gly	Ala	Arg	Leu	Val	Val	Leu	Ala	Thr	Ala	Thr	Pro	Pro	
195					530					535					540		
197	gga	tcg	gtc	acc	gtg	cca	cat	cca	aac	atc	gag	gag	gtg	gct	ctg	tcc	3479
198	Gly	Ser	Val	Thr	Val	Pro	His	Pro	Asn	Ile	Glu	Glu	Val	Ala	Leu	Ser	
199					545					550					555		
201	agc	act	gga	gaa	atc	ccc	ttt	tat	ggc	aaa	gcc	atc	ccc	atc	gag	acc	3527
202	Ser	Thr	Gly	Glu	Ile	Pro	Phe	Tyr	Gly	Lys	Ala	Ile	Pro	Ile	Glu	Thr	
203	560					565					570					575	
205	atc	aag	ggg	ggg	agg	cac	ctc	att	ttc	tgc	cat	tcc	aag	aag	aaa	tgt	3575
206	Ile	Lys	Gly	Gly	Arg	His	Leu	Ile	Phe	Cys	His	Ser	Lys	Lys	Lys	Cys	
207					580						585					590	
209	gat	gag	ctc	gcc	gcg	aag	ctg	tcc	ggc	ctc	gga	ctc	aat	gct	gta	gca	3623
210	Asp	Glu	Leu	Ala	Ala	Lys	Leu	Ser	Gly	Leu	Gly	Leu	Asn	Ala	Val	Ala	
211					595					600					605		
213	tat	tac	cgg	ggc	ctt	gat	gta	tcc	gtc	ata	cca	act	agc	gga	gac	gtc	3671
214	Tyr	Tyr	Arg	Gly	Leu	Asp	Val	Ser	Val	Ile	Pro	Thr	Ser	Gly	Asp	Val	
215					610					615					620		
217	att	gtc	gta	gca	acg	gac	gct	cta	atg	acg	ggc	ttt	acc	ggc	gat	ttc	3719
218	Ile	Val	Val	Ala	Thr	Asp	Ala	Leu	Met	Thr	Gly	Phe	Thr	Gly	Asp	Phe	
219					625						630				635		
221	gac	tca	gtg	atc	gac	tgc	aat	aca	tgt	gtc	acc	cag	aca	gtc	gac	ttc	3767
222	Asp	Ser	Val	Ile	Asp	Cys	Asn	Thr	Cys	Val	Thr	Gln	Thr	Val	Asp	Phe	
223	640					645					650					655	
225	agc	ctg	gac	ccg	acc	ttc	acc	att	gag	acg	acg	acc	gtg	cca	caa	gac	3815
226	Ser	Leu	Asp	Pro	Thr	Phe	Thr	Ile	Glu	Thr	Thr	Thr	Val	Pro	Gln	Asp	
227					660						665					670	
229	gcg	gtg	tca	cgc	tcg	cag	cgg	cga	ggc	agg	act	ggg	agg	ggc	agg	atg	3863
230	Ala	Val	Ser	Arg	Ser	Gln	Arg	Arg	Gly	Arg	Thr	Gly	Arg	Gly	Arg	Met	
231					675					680					685		
233	ggc	att	tac	agg	ttt	gtg	act	cca	gga	gaa	cgg	ccc	tcg	ggc	atg	ttc	3911
234	Gly	Ile	Tyr	Arg	Phe	Val	Thr	Pro	Gly	Glu	Arg	Pro	Ser	Gly	Met	Phe	
235					690					695					700		
237	gat	tcc	tcg	gtt	ctg	tgc	gag	tgc	tat	gac	gcg	ggc	tgt	gct	tgg	tac	3959
238	Asp	Ser	Ser	Val	Leu	Cys	Glu	Cys	Tyr	Asp	Ala	Gly	Cys	Ala	Trp	Tyr	
239					705					710					715		
241	gag	ctc	acg	ccc	gcc	gag	acc	tca	gtt	agg	ttg	cgg	gct	tac	cta	aac	4007
242	Glu	Leu	Thr	Pro	Ala	Glu	Thr	Ser	Val	Arg	Leu	Arg	Ala	Tyr	Leu	Asn	
243	720					725					730					735	
245	aca	cca	ggg	ttg	ccc	gtc	tgc	cag	gac	cat	ctg	gag	ttc	tgg	gag	agc	4055
246	Thr	Pro	Gly	Leu	Pro	Val	Cys	Gln	Asp	His	Leu	Glu	Phe	Trp	Glu	Ser	

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247		740		745		750		
249	gtc ttt aca ggc ctc acc cac ata gac gcc cat ttc ttg tcc cag act							4103
250	Val Phe Thr Gly Leu Thr His Ile Asp Ala His Phe Leu Ser Gln Thr							
251		755		760		765		
253	aag cag gca gga gac aac ttc ccc tac ctg gta gca tac cag gct acg							4151
254	Lys Gln Ala Gly Asp Asn Phe Pro Tyr Leu Val Ala Tyr Gln Ala Thr							
255		770		775		780		
257	gtg tgc gcc agg gct cag gct cca cct cca tcg tgg gac caa atg tgg							4199
258	Val Cys Ala Arg Ala Gln Ala Pro Pro Pro Ser Trp Asp Gln Met Trp							
259		785		790		795		
261	aag tgt ctc ata cgg cta aag cct acg ctg cac ggg cca acg ccc ctg							4247
262	Lys Cys Leu Ile Arg Leu Lys Pro Thr Leu His Gly Pro Thr Pro Leu							
263	800		805		810		815	
265	ctg tat agg ctg gga gcc gtt caa aac gag gtt act acc aca cac ccc							4295
266	Leu Tyr Arg Leu Gly Ala Val Gln Asn Glu Val Thr Thr Thr His Pro							
267		820		825		830		
269	ata acc aaa tac atc atg gca tgc atg tcg gct gac ctg gag gtc gtc							4343
270	Ile Thr Lys Tyr Ile Met Ala Cys Met Ser Ala Asp Leu Glu Val Val							
271		835		840		845		
273	acg agc acc tgg gtg ctg gta ggc gga gtc cta gca gct ctg gcc gcg							4391
274	Thr Ser Thr Trp Val Leu Val Gly Gly Val Leu Ala Ala Leu Ala Ala							
275		850		855		860		
277	tat tgc ctg aca aca ggc agc gtg gtc att gtg ggc agg atc atc ttg							4439
278	Tyr Cys Leu Thr Thr Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu							
279		865		870		875		
281	tcc gga aag ccg gcc atc att ccc gac agg gaa gtc ctt tac cgg gag							4487
282	Ser Gly Lys Pro Ala Ile Ile Pro Asp Arg Glu Val Leu Tyr Arg Glu							
283	880		885		890		895	
285	ttc gat gag atg gaa gag tgc gcc tca cac ctc cct tac atc gaa cag							4535
286	Phe Asp Glu Met Glu Glu Cys Ala Ser His Leu Pro Tyr Ile Glu Gln							
287		900		905		910		
289	gga atg cag ctc gcc gaa caa ttc aaa cag aag gca atc ggg ttg ctg							4583
290	Gly Met Gln Leu Ala Glu Gln Phe Lys Gln Lys Ala Ile Gly Leu Leu							
291		915		920		925		
293	caa aca gcc acc aag caa gcg gag gct gct gct ccc gtg gtg gaa tcc							4631
294	Gln Thr Ala Thr Lys Gln Ala Glu Ala Ala Ala Pro Val Val Glu Ser							
295		930		935		940		
297	aag tgg cgg acc ctc gaa gcc ttc tgg gcg aag cat atg tgg aat ttc							4679
298	Lys Trp Arg Thr Leu Glu Ala Phe Trp Ala Lys His Met Trp Asn Phe							
299		945		950		955		
301	atc agc ggg ata caa tat tta gca ggc ttg tcc act ctg cct ggc aac							4727
302	Ile Ser Gly Ile Gln Tyr Leu Ala Gly Leu Ser Thr Leu Pro Gly Asn							
303	960		965		970		975	
305	ccc gcg ata gca tca ctg atg gca ttc aca gcc tct atc acc agc ccg							4775
306	Pro Ala Ile Ala Ser Leu Met Ala Phe Thr Ala Ser Ile Thr Ser Pro							
307		980		985		990		
309	ctc acc acc caa cat acc ctc ctg ttt aac atc ctg ggg gga tgg gtg							4823
310	Leu Thr Thr Gln His Thr Leu Leu Phe Asn Ile Leu Gly Gly Trp Val							
311		995		1000		1005		

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:2; Xaa Pos. 882,1489

Seq#:3; Xaa Pos. 882,1489

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L:11 M:270 C: Current Application Number differs, Replaced Current Application No  
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:631 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:2  
L:635 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:2  
L:887 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:4489  
M:341 Repeated in SeqNo=2  
L:1237 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3  
L:1348 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:880  
M:341 Repeated in SeqNo=3